

DATE: 06/04/2002

TIME: 15:53:49

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		Input Set : A:\701586sq Output Set: N:\CRF3\06042002\1701586B.raw														
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			Otter													ENTERED
	6 7		Lubis													
			Lemai	-												
	8	<120×	TITLE													
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						ON: pr	oduct	t is	Poly	ADI	Rib	ose	Poly	mera	ıse;	from brain tissue
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						g cga										47
	37 38		с Ата. 1	Ald A	ig Al	g Arg	Arg :	ser .	IIII (	10	эт У	эт Х т	119 2	ııa r	15	
			_	паа	age a	aa aga	att	aat	aat		aac	асσ	act	cca		95
						ys Arg										
	42		· · · · · · · · · · · · · · · · · · ·		20	.10 3			25	1				30		
		gac t	ct tcc	cct		ag aaa	act	cqt	aga	tgc	caq	aga	caq	gag	tcg	143
						ys Lys										
	46	-		35				40					45			
	48	aaa a	ag atg	cct	gtg g	rct gga	gga	aaa	gct	aat	aag	gac	agg	aca	gaa	191
	49	Lys L	ys Met	Pro	Val A	la Gly	Gly	Lys	Ala	Asn	Lys	Asp	Arg	Thr	Glu	L
	50		50				55					60			•	•
		-	-	_	-	ct gtg	_	_	_	-		_				
		-	_	Asp	Glu S	er Val	_	Ala	Leu	Leu		Lys	Gly	Lys	Ala	ι .
	54		65			70					75					
						gt aca										
			al Asp	Pro		ys Thr	Ala	Lys	Val		Lys	Ala	His	Val		
		80				85				90					95	
						tc tat										
	61	Cys G	⊥u GIY	Asn	Asp V	al Tyr	Asp	val	met	Leu	Asn	GIn	rnr	Asn	тец	l

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,586B

RAW SEQUENCE LISTING DATE: 06/04/2002 PATENT APPLICATION: US/09/701,586B TIME: 15:53:49

Input Set : A:\701586sq

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	96 97 98 100 101 102 104 105	Glu 240 aag Lys att	atg Met ctg Leu	Met g aca g Thi	Met gtg Val	Glu gca Ala 260 att	Met 245 caa Gln	aag Lys atc Ile	Tyr : aag : Lys : ggc	Asn gca Ala cag Gln	ggt Gly 265 Cat	Lys 250 tac Tyr	aaa Lys cag Gln	Ala f tct n Sei n-gct	Pro ctt Leu cto	Leu Lys 270 ato	Gly 255 g aag s Lys	815	
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	96 97 98 100 101 102 104 105 106 108 110 112	Glu 240 aag Lys att Ile	atg Met  g ctg Let  g ag  g Gli  t tgc  t Cys	Met g aca t Thi g gat t Asp c aat s Asr 290 c cca	Met  gtg Val  tgt Cys 275 gaa Glu  cta	Glu gca Ala 260 att Ile tto	Met 245 caa Gln cgg Arg	aag Lys atc Ile gct Ala acc	Tyr aag Lys Gly agg Arg 295	Asn gca Ala cag Gln 280 att Ile	Thr ggt Gly 265 cat His	Lys 250 tac Tyr gga Gly cat His	aaa Lys cag Glm cga Arg	Ala y tot y Ser y Ala y ttt y Ala y Phe 300	Pro  ctt Leu 285 cgga cGly	Leu  aag 1 Lys 270 2 atc 3 Met 5 Leu 1 ata	Gly 255 y aag s Lys ) y gaa c Glu c cgt n Arg	863	
	96 97 98 100 101 102 104 105 106 108 110 112	Glu 240 aac Lys att Ile Gca Ala act	atg Met  g ctg S Let c gag e Glu c tgc c Cys c cct	Met g aca g Thi g gat i Asp c aat s Asr 290 c Cca o Pro	Met  gtg Val  tgt Cys 275 gaa Glu  cta	Glu gca Ala 260 att Ile tto	Met 245 caa Gln cgg Arg	aag Lys atc Ile gct Ala acc Thr	Tyr aag Lys Gly agg Arg 295 cag	Asn gca Ala cag Gln 280 att Ile	Thr ggt Gly 265 cat His	Lys 250 tac Tyr gga Gly cat His	aaa Lys cag Glm cga Arg	Ala y tot y Ser y Ala y ttt y Phe 300 y gaa c Gli	Pro  ctt Leu 285 cgga cGly	Leu  aag 1 Lys 270 2 atc 3 Met 5 Leu 1 ata	Gly 255 y aag s Lys y gaa c Glu c cgt n Arg	815 863 911	
	96 97 98 100 101 102 104 105 106 108 119 111 113	Glu 240 aag Lys att Ile Gaa Ala	atg Met G Leu G Leu G Cys C Cys C Cys 305	Met g aca g at g at l Asp c aat s Asr 290 c cca c Pro	Met  gtg Val  tgt Cys 275 gaa Glu  Leu	Glu gca Ala 260 att Ile tto	Met 245 caa Gln cgg Arg Tyr cgg Arg	aag Lys atc Ile gct Ala acc Thr	Tyr aag Lys Gly agg Arg 295 cag	gca Ala Cag Gln 280 att Ile aag	ggt Gly 265 cat His ccg Pro	Lys 250 tac Tyr gga Gly cat His	aaa Lys cag Glm cga Arg Asp	Ala y tot y Ser y Ala y Ala y tot y Ala y Ala y Gli y Gli y	Pro ctt Leu ctc Leu 285 cgga cgga cgga cgga cgga cgga cgga cgg	Leu  c aac  l Lys  270  c atc  Met  Leu  t ata  s Ile	Gly 255 3 aag 4 Lys 5 Lys 6 Glu 7 Gaa 7 Glu 8 cgt 8 Arg 8 Caa	815 863 911 959	
	96 97 98 100 101 102 104 105 106 108 119 1113 114 116	Glu 240 aac Lys att Ile Gaac Ala	atg Met  g ctg S Let  gag Glu  tg Cys cct Type S Cot S Cys cct Type S Cot S Cys	Met  g aca  g at  Asp  c aat  s Asr  290  c cca  pro	Met  gtg Val  tgt Cys 275 gaa Glu  Leu gget	Glu  gca Ala 260 att Ile tto Phe atc	Met 245 Caaa Gln Cgg Arg Tyr Cgg Arg	aag Lys atc Ile Ala acc Thr aca Thr 310	Tyr aagg Gly agg Arg 295 Cag Gln	Asn gca Ala Cag Gln 280 att Ile aag Lys	Thr ggt Gly 265 cat His ccg Pro	Lys 250 tac Tyr gga Gly cat His	aaa Lys cag Glm cga Arg Asp tca Ser 315	Ala y tot y Ser y Ala y Ala y Ala y Ala y Ala y Gli y Gli y Ala	Pro ctt ctc ctc ctc ctc csc csc csc csc csc	Leu  aag 1 Lys 270 2 atg 1 Met 3 tata 3 Ile	Gly 255 3 aag 5 Lys 6 Glu 7 cgt 1 Arg 8 Caa 8 Gln 9 aaa	815 863 911	
	96 97 98 100 101 102 104 105 106 108 110 112 113 114 116	Glu 240 aag Lys att Ile Gat Ala Ala tta	atg Met  g ctg S Leu  gag Glu  t ctg C Pro 305 c cta Leu Leu Leu	Met  g aca  g at  Asp  c aat  s Asr  290  c cca  pro	Met  gtg Val  tgt Cys 275 gaa Glu  cta Leu gget	Glu  gca Ala 260 att Ile tto Phe atc	Met 245 Caa Gln Cgg Arg Tyr Cgg Arg	aag Lys atc Ile Ala acc Thr aca Thr 310 gac	Tyr aagg Gly agg Arg 295 Cag Gln	Asn gca Ala Cag Gln 280 att Ile aag Lys	Thr ggt Gly 265 cat His ccg Pro	Lys 250 tac Tyr gga Gly cat His	aaa Lys cag Glm cga Arg Asp tca Ser 315	Ala y tot y Ser y Ala y Ala y Ala y Ala y Gli y Gli y Ala	Pro ctt ctc ctc ctc ctc csc csc csc csc csc	Leu  aag 1 Lys 270 2 atg 1 Met 5 1 cto 7 Leu 1 ata 5 Ile	Gly 255 3 aag 5 Lys 6 gaa 7 Glu 7 Caa 8 Gln 9 aaa 8 Lys	815 863 911 959	
	96 97 98 100 101 102 104 105 106 108 119 110 1113 114 116 117 118	att Ile	atg Met  g ctg G Leu  c gag G Glu  c Cys c Cys c ctc 305 c cta Leu )	Met g aca g at g As a at s As c cat s As c pro c cca g ac g ac g ac g ac g ac g ac g a	Met  gtg Val  tgt Cys 275 gaa Glu cta Leu gct Ala	Glu  gca Ala 260 att Ile tto Phe atc	Met 245 Caaa Gln Cgg Arg Tyr Cgg Arg Gly Gly 325	aag Lys atc Ile gct Ala acc Thr aca Thr 310 gac Asp	aag Lys Gly agg Arg 295 Cag Cag	Asn gca Ala Cag Gln 280 att Ile aag Lys gaa Glu	ggt Gly 265 cat His ccg Pro	Lys 250 tac Tyr gga Gly cat His cto Leu gct Ala 330	aaa Lys cag Glm cga Arg Asp tca Ser 315	Ala y tot y Ser y Ala y tot y Ala y Ala y Ett y Ala	Pro  ctt ctc Let 285 cgga cgga cgly aaaa ctg	Leu Laag Lys 270 Catg Met Leu	Gly 255 3 aag 5 Lys 6 gaa 7 Glu 7 Caa 8 Gln 9 aaa 8 Lys 335	815 863 911 959 1007	
	96 97 98 100 101 102 104 105 106 108 119 1113 114 116 117 118 120	att Ile	atg Met  g ctg G Leu  c gag G Cys c ctg G Cys c ctg G Cys c ctg G Cys G	Met  g aca  g at  g at  aat  As  290  C cca  pro  i gag  i Gli  g cta	Met  gtg Val  tgt Cys 275 gaa Glu cta Leu gct Ala	Glu  gca Ala 260 att Ile tto Interpretation Leu ago	Met 245 Caa Gln Cgg Arg Tyr Cgg Arg Gly 325 Cca	aag Lys atc Ile Ala acc Thr aca Thr 310 gac Asp	Tyr aag Lys Gly agg Arg 295 Cag Tile	Asn gca Ala cag Gln 280 att Ile aag Lys gaa Glu cca	Thr ggt Gly 265 cat His ccg Pro gaa Glu att	Lys 250 tac Tyr gga Gly cat His cto gct Ala 330 gac	aaa Lys cag Glm cga Arg Asp tca Ser 315 att	Ala y tot y Ser y Ala y tot y Ala y tot y Ala y	Pro  ctt ctc ctc ctc csc csc csc csc csc cs	Leu  aag 1 Lys 270 a to 1 Met 1 cto 2 Leu 1 ata 3 Ile 3 gto 1 Val	Gly 255 3 aag 5 Lys 7 gaa 6 Glu 7 cgt 1 Arg 1 caa 8 Gln 1 aaa 1 Lys 335 1 aac	815 863 911 959	
	96 97 98 100 101 102 104 105 106 108 119 1113 114 116 117 118 120	att Ile Ala Ala Leu 320 aca Thr	atg Met  g ctg G Leu  c gag G Cys c ctg G Cys c ctg G Cys c ctg G Cys G	Met  g aca  g at  g at  aat  As  290  C cca  pro  i gag  i Gli  g cta	Met  gtg Val  tgt Cys 275 gaa Glu cta Leu gct Ala	Glu  gca Ala 260 att Ile tto Interpretation Leu ago	Met 245 Caaa Gln Cgg Arg Tyr Cgg Arg Gly 325 Ccaa	aag Lys atc Ile Ala acc Thr aca Thr 310 gac Asp	Tyr aag Lys Gly agg Arg 295 Cag Tile	Asn gca Ala cag Gln 280 att Ile aag Lys gaa Glu cca	Thr ggt Gly 265 cat His ccg Pro gaa Glu att	Lys 250 tac Tyr gga Gly cat His cto Let gct Ala 330 gac Asr	aaa Lys cag Glm cga Arg Asp tca Ser 315 att	Ala y tot y Ser y Ala y tot y Ala y tot y Ala y	Pro  ctt ctc ctc ctc csc csc csc csc csc cs	Leu  aag 1 Lys 270 a to 1 Met 1 cto 2 Leu 1 ata 3 Ile 3 gto 1 Val	Gly 255 3 aag 5 Lys 7 gaa 6 Glu 7 caa 8 Gln 8 aaa 9 Lys 335 1 aaa 9 Asn	815 863 911 959 1007	
	96 97 98 100 101 102 104 105 106 108 119 111 113 114 116 117 118 120 121	att Ile Alact Thr	atg Met  g ctg Leu  gag Glu  ctg Cys cta Cys cta Leu  gag Glu  gag Glu	Met g aca g at a As a As a Co c	Met  gtg Val  tgt Cys 275 gaa Glu  cta Leu gct Ala	gca Ala 260 att Ile tto Phe atc Leu ago Ser 340	Met 245 Caaa Gln Cgg Arg Tyr Cgg Arg Cgg Arg Cgg Arg	aag Lys atc Ile gct Ala acc Thr aca Thr 310 gac Asp	Tyr aag Lys Gly agg Arg 295 Cag Gln att	Asn gca Ala Cag Gln 280 att Ile aag Lys gaa Glu cca Pro	Thr  ggt Gly 265 cat His ccg Pro gaa Glu att Ile ttg Leu 345	Lys 250 tac Tyr gga Gly cat His cto Let gct Ala 330 gac Asp	aaa Lys cag Gln cga Arg Asp tca Ser 315	Ala y tot y Ser y Ala y tot y Ala y	Pro  ctt ctt ctc ctc ctc csc csc csc csc cs	Leu Laag 270 Leu	Gly 255 3 aag 5 Lys 7 gaa 6 Glu 7 caa 8 Gln 8 aaa 9 Gln 9 aaa 1 Lys 335 1 aac 9 Asn	815 863 911 959 1007	
	96 97 98 100 101 102 104 105 108 109 110 113 114 116 117 118 120 121 122 124	att Ile Alact Thr	Met  Goto Goto Goto Goto Goto Goto Goto G	Met g aca g ata g ata s Asr 290 c cca p Pro i gag g cta g cta g cta t tgt	Met  gtg Val  tgt Cys 275 gaa Glu  Leu gct Ala caa Glr	Glu  gca Ala 260 att Ile tto Phe atc Ile Ser 340 ttg	Met 245 Caaa Gln Cgg Arg Tyr Cgg Arg Gly Gly Cca Pro	aag Lys atc Ile gct Ala acc Thr aca Thr 310 gac Asp	Tyr aagg Lys Gly agg Arg 295 Cag Gln att	Asn gca Ala Cag Gln 280 att Ile aag Lys gaa Glu cca pro	Thr ggt Gly 265 cat His ccg Pro gaa Glu att Ile ttg Leu 345 cat	Lys 250 tac Tyr gga Gly cat His cto Leu gct Ala 330 gac Asp	aaa Lys cag Gln cga Arg Asp tca Ser 315 att Ile	Ala y tot y Ser y Ala y tot y Ala y	Pro  c ctt c Leu c 285 c gga e Gly a aaa i Lys g ctg c tat c tat c gag	Leu  Leu  Leu  270  270  Met  Control  Leu  Arg  350  tto	Gly 255 3 aag 5 Lys 7 gaa 6 Glu 7 caa 8 Gln 8 aaa 9 Lys 335 1 aaa 9 Asn	815 863 911 959 1007 1055	

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13			385					390					395					
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		_	Glu	Ala	Phe	Arg		Asp	Leu	His	Asn			Leu	Leu	Trp		
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				+ ~+	a a +	~~~	ata		~~~	aaa	22+	aat		gcc	as s	aas	++~	1487
	-	-	_	_		_				-			-	Ala	-			1407
	8 4	-	GIII	Cys	ASII	GIU	485	пеп	Giu	AIG	ASII	490	пуз	АΙα	Giu	GLY	495	
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							_		_		_		_	Met	-		-	1333
16			0	<b>υ</b> Δ1	2,0	500			_10	0,21	505	1	-10			510		
		ct	acc	cac	ttc		acc	cta	aat	aga		aca	ata	cca	tta		cca	1583
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16					515					520					525	-		
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16	9 A	la	ser	Asp	Thr	Gly	Ile	Leu	Asn	Pro	Asp	Gly	Tyr	Thr	Leu	Asn	Tyr	
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			-					Phe	Leu	Gln	Leu	-						
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																	gaatt	1785
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					H: 57	/0												
				PE:														
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					NCE:				<b>a</b> .	m1	a 1	<b>a</b> 3	<b>a</b> 3				3.1-	
			Ala	Ala	Arg	_	Arg	Arg	ser	Thr		GIY	GLY	Arg	Ala	_	AIA	
	3		3 c	<b>01.</b>	0	5	A	77 n 7	<b>3</b> ~ ~	7	10	N	m 1	A 7 -	D	15	3.00	
19	э Г	eu	Asn	GIU	ser	гĀ2	arg	val	ASN	ASN	GTĀ	ASN	Thr	Ala	PLO	GIU	Asp	

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	208					85					90					95			
		Glu	Gly	Asn	Asp	Val	$\mathtt{Tyr}$	Asp	Val		Leu	Asn	Gln	Thr	Asn	Leu	Gln		
	211				100					105	_				110		_		
		Phe	Asn		Asn	_	_	_		Ile	Gln	Leu	Leu	Glu	Asp	Asp	Ala		
	214	_		115	_				120		_			125		_			
		Gln	_	Asn	Phe	Ser	Val	_	Met	Arg	Trp	GLY		Val	GLY	Lys	Met		
	217		130	•	_			135		<b>~</b>	<b>a</b> 1		140	•	<b>.</b>		-		
		_		His	ser	Leu		Ата	Cys	Ser	GLY		Leu	Asn	ьys	Ala	_		
		145		<b>D</b> 1	a1	<b>.</b>	150	Dl	<b>.</b>		<b>-</b>	155	<b>T</b>	3	<b>3</b>		160		
		GIU	ше	Pne	Gin	_	гÀг	Pne	ьeu	Asp	_	Thr	ьys	Asn	ASN	_	GIU		
	223	3	7	C1	T	165	C1	T ***	Vol	Dwo	170	T ***	Ш	N an	Wot	175	Cln		
	225	Asp	Arg	GIU	180	Phe	GIU	гуѕ	Val	185	СТА	гая	TYL	Asp	190	Leu	GIII		
		Wot	7 00	Ш.т.т		mh r	N a n	Thr	Cln		Clu	Clu	Clui	Thr		Tara	Clu		
	229	Met	нар	195	нта	1111	ASII	TIIT	200	waħ	Giu	GLu	Gru	205	пуз	пуэ	GIU		
		Glu	Sar	-	T.v.c	Sar	Dro	T.e.ii		Pro	Glu	Ser	Gln	Leu	Δen	T.e.ii	Δrα		
	232	Gru	210	пеп	цуэ	Per	FIU	215	пуз	FIO	GIU	SCI	220	пеа	изр	ЦСu	ALG		
		Va 1		Glu	T.e.11	Tle	T.v.c		Tle	Cvs	Δsn	Va 1		Ala	Met	Glu	Glu		
		225	OIII	Oiu	Dea	110	230	11Cu	110	0,0	11011	235	01			014	240		
			Met	Met	Glu	Met		Tvr	Asn	Thr	Lvs		Ala	Pro	Leu	Glv			
	238					245	-1-	-1-			250	-1-				255	-1-		
		Leu	Thr	Val	Ala		Ile	Lvs	Ala	Glv		Gln	Ser	Leu	Lys		Ile		
	241			,	260			-4-		265					270	4 -	_		
		Glu	Asp	Cys	Ile	Arg	Ala	Gly	Gln	His	Gly	Arg	Ala	Leu	Met	Glu	Ala	 ~	 
	244		-	275		-		-	280		_	_		285					
	246	Cys	Asn	Glu	Phe	Tyr	Thr	Arg	Ile	Pro	His	Asp	Phe	Gly	Leu	Arg	Thr		
	247	_	290			-		295					300						
	249	Pro	Pro	Leu	Ile	Arg	Thr	Gln	Lys	Glu	Leu	Ser	Glu	Lys	Ile	Gln	Leu		
	250	305					310					315					320		
	252	Leu	Glu	Ala	Leu	Gly	Asp	Ile	$\operatorname{Glu}$	Ile	Ala	Ile	Lys	Leu	Val	Lys	Thr		
	253					325					330					335			
		Glu	Leu	Gln		${\tt Pro}$	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg	Asn	Leu		
	256				340					345					350				
•		His	Cys		Leu	Arg	Pro	Leu			Glu	Ser	Tyr	Glu	Phe	Lys	Val		
	259			355					360					365					
				Gln	$\mathtt{Tyr}$	Leu	Gln		Thr.	His	Ala	Pro		His	Ser	Asp	Tyr		
	262		370					375					380						
			Met	Thr	Leu	Leu		Leu	Phe	Glu	Val		Lys	Asp	Gly	Glu	_		
		385					390					395					400		
	267	Glu	Ala	Phe	Arg	Glu	Asp	Leu	His	Asn	Arg	Met	Leu	Leu	$\mathtt{Trp}$	His	Gly		

410

405

268

RAW SEQUENCE LISTING DATE: 06/04/2002 PATENT APPLICATION: US/09/701,586B TIME: 15:53:49

Input Set : A:\701586sq

Output Set: N:\CRF3\06042002\1701586B.raw

	Ser	Arg	Met		Asn	Trp	Val	Gly	Ile	Leu	Ser	His	Gly	Leu	Arg	Ile				
271				420					425					430						
273	Ala	Pro		Glu	Ala	Pro	Ile		Gly	Tyr	Met	Phe	${\tt Gly}$	Lys	Gly	Ile				
274			435					440		_			445						•	
	Tyr		Ala	Asp	Met	Ser		Lys	Ser	Ala	Asn		Cys	Phe	Ala	Ser				
277	_	450	_	_			455	_	_	_	_	460			_					
		Leu	гля	Asn	Thr	-	Leu	Leu	Leu	Leu		GIU	Val	ALa	Leu	_				
	465	<b>~</b>		<b>a</b> 1	T	470	<b>a</b> 1			D	475	.1-	<b>01</b>	<b>63</b>	<b>T</b>	480				
	GIN	Cys	ASn	GIU		Leu	Glu	Ala	ASN		гаг	Ala	Glu	GLY		Leu				
283	Cln	C1**	T 110	Hic	485	Πh~	T ***	C1**	T 011	490	T ***	Wat	Ala	Dro	495	Con				
286	GIII	GIA	пур	500	ser	1111	nys	СТА	505	GIY	пуъ	Met	нта	510	ser	Set				
	Δla	His	Phe		Thr	Len	Δgn	Glv		Thr	Val	Pro	Leu		Pro	Δla				
289	1124		515	, 42		шей	21011	520	00-	1 ***	, u _	110	525	OL J	110	ALG				
	Ser	Asp		Glv	Ile	Leu	Asn		Asp	Glv	Tvr	Thr	Leu	Asn	Tvr	Asn				
292		530		1			535			2	-1-	540			- 4 -					
	Glu	Tyr	Ile	Val	Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu	Leu				
295		_			-	550					555		_	•		560	•			
297	Lys	Val	Gln	Phe	Asn	Phe	Leu	Gln	Leu	Trp					•					
298					565					570										
301	<210	)> SI	EQ II	ON C	: 3												•			
				I: 22	265															
	<212															•			•	
				SM:	Homo	sap	piens	3												
	<220																			
				KEY:																
				ON:					_ 4 _	Do.1-	- 301	n n/1		D-1-			·			
				INFC		LION	; pro	oauci	LIS	POL	ADI	KII	oose	POT	mera	ıse; I	rom ute	rus t	ıssue	
						-c a	reete	10000	- aa	acto	act	toad	20002	act c	ratar	jccaaa	. 60	า		
																gaatto				
																gggag				
																ettgge				
							_	_	-			-	ag gg	_			286			
322													lu G							
323		1				5				:	LO			_	1	L5				
													CCC				334	1		
													Pro							
													cgc				382	2		
	Thr	Ala	Glu		Leu	Lys	Ala	Ile		Ala	Glu	Lys	Arg		Ile	Arg				
331				35					40					45						
													acc				430	)		
	Val	Asp		Thr	Cys	Pro	Leu		Ser	Asn	Pro	GLY	Thr	GLn	Val	Tyr				
335	~		50		<b>.</b>		_+-	55				_4-	60				4 4	_		
													gag				478	3		
	GIU	_	ryr	ASN	cys	Tnr		ASN	GIN	Tnr	ASN		Glu	ASN	ASN	ASN				
339	224	65	++~	+	2+~	2+~	70	a+~	at a		~~~	75	222	000	++-	++~	E 0.4	e		
74T	aac	aay	LLC	Lac	all	all	cay	CLG	CLC	caa	yac	ayc	aac	cyc	LLC	LLC	526	כ	•	

RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/09/701,586B

DATE: 06/04/2002 TIME: 15:53:50

Input Set : A:\701586sq

Output Set: N:\CRF3\06042002\1701586B.raw

## Please Note:

Seq#:11; Xaa Pos. 2,3,4,5,6,7,9,10,11

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:12; Xaa Pos. 1,2,6,7,9,10,11,12,13,14,16,17,18
Seq#:13; Xaa Pos. 6,7,8,9,10,11,12,13,16,17,21,22,24,25,26,27,28,29,31,32
Seq#:13; Xaa Pos. 33,41,42,43,48
Seq#:14; Xaa Pos. 1,2,3,4,5,6,7,9,10,11,12,13,14,16,17,18,19,20,21
Seq#:15; Xaa Pos. 2,3,4,5,6,7,8,9,10,12,13,15,16,20,21,22,23,24,25,26,27,28
Seq#:15; Xaa Pos. 29,30,31,32
Seq#:16; Xaa Pos. 2,3,4,6,8,9,10,11,14,16,18,19,20,21,22,24,25,26,28
Seq#:17; Xaa Pos. 2,4,5,6,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23,24,25
Seq#:17; Xaa Pos. 26,27,33,34,35,38,39,40,41,42,43
Seq#:18; Xaa Pos. 4,8,11,12,13
Seq#:19; Xaa Pos. 2,3,4,6,7,9,13,15,16
Seq#:20; Xaa Pos. 2,3,4,6
Seq#:21; Xaa Pos. 2,3,5,6,7,8,10,11,12,14,15,16,17,18,19,20,21,22,24,26,27
Seq#:22; Xaa Pos. 2,3,4,6,7,8,10,11,12,13
Seq#:29; Xaa Pos. 2,3,4
Seq#:30; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:30; Xaa Pos. 24,25,26,27,28,29,30,31,32,33,34,36,37
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